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Reviewer: Anne Corrigan
Timestamp: Fri Nov 02 14:26:43 EDT 2007
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Application No: 10592944   Version No: 1.0

Input Set:

Output Set:

Started:	2007-10-18 13:49:33.374
Finished:	2007-10-18 13:49:34.851
Elapsed:	0 hr(s) 0 min(s) 1 sec(s) 477 ms
Total Warnings:	25
Total Errors:	0
No. of SeqIDs Defined:	26
Actual SeqID Count:	26

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
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W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

Input Set:

Output Set:

Started:	2007-10-18 13:49:33.374
Finished:	2007-10-18 13:49:34.851
Elapsed:	0 hr(s) 0 min(s) 1 sec(s) 477 ms
Total Warnings:	25
Total Errors:	0
No. of SeqIDs Defined:	26
Actual SeqID Count:	26

Error code   Error Description

This error has occured more than 20 times, will not be displayed

<110> BOUGERET, CECILE
      ZARZOV, PATRICK
      BRIAND, JEAN-FRANCOIS
      THOMAS, DOMINIQUE

<120> METHOD FOR SCREENING AGENTS MODULATING I-KAPPA B-ALPHA
      PROTEIN UBIQUITINATION AND MEANS FOR CARRYING OUT SAID
      METHOD

<130> 0510-1149

<140> 10592944
<141> 2007-10-18

<150> PCT/FR05/050165
<151> 2005-03-15

<150> FR 04 50528
<151> 2004-03-16

<160> 26

<170> PatentIn Ver. 3.3

<210> 1
<211> 1719
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

<400> 1
atgtctaaag gtgaagaatt attcactggt gttgtcccaa ttttggttga attagatggt 60
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gtcactactt tcggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240
catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tatttttttc 300
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ttggaataca actataactc tcacaatgtt tacatcatgg ctgacaaaca aaagaatggt 480
atcaaagtta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 540
cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 600
ttatccactc aatctgcctt atccaaagat ccaaacgaaa agagagacca catggtcttg 660
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agcccacctc caaaaaagaa gagaaaggtc gaattgggcg gatccatgtt ccaggcggcc 780
gagcgccccc aggagtgggc catggagggc ccccgcgacg ggctgaagaa ggagcggcta 840
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tgtctacact tagcctctat ccatggctac ctgggcatcg tggagctttt ggtgtccttg 1380
ggtgctgatg tcaatgctca ggagccctgt aatggccgga ctgcccttca cctcgcagtg 1440
gacctgcaaa tcctgacct ggtgtcactc ctgttgaagt gtggggctga tgtcaacaga 1500
gttacctacc agggctattc tccctaccag ctcacctggg gccgcccaag cacccggata 1560
cagcagcagc tgggccagct gacactagaa aaccttcaga tgctgccaga gagtgaggat 1620
gaggagagct atgacacaga gtcagagttc acggagttca cagaggacga gctgccctat 1680
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<210> 2
<211> 572
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     construct

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
             20                  25                  30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
         35                  40                  45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
 65                  70                  75                  80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                 85                  90                  95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
             100                 105                 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
         115                 120                 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
     130                 135                 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                 165                 170                 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
             180                 185                 190
```

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195   200   205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210   215   220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Gln
225   230   235   240

Ser Pro Pro Pro Lys Lys Arg Lys Val Glu Leu Gly Gly Ser Met
                245   250   255

Phe Gln Ala Ala Glu Arg Pro Gln Glu Trp Ala Met Glu Gly Pro Arg
                260   265   270

Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His Asp Ser Gly
        275   280   285

Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys Glu Leu
        290   295   300

Gln Glu Ile Arg Leu Glu Pro Gln Glu Val Pro Arg Gly Ser Glu Pro
305   310   315   320

Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu Ala
                325   330   335

Ile Ile His Glu Glu Lys Ala Leu Thr Met Glu Val Ile Arg Gln Val
        340   345   350

Lys Gly Asp Leu Ala Phe Leu Asn Phe Gln Asn Asn Leu Gln Gln Thr
        355   360   365

Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Glu Ile Ala Glu Ala
370   375   380

Leu Leu Gly Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg Gly Asn
385   390   395   400

Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val Gly
                405   410   415

Val Leu Thr Gln Ser Cys Thr Thr Pro His Leu His Ser Ile Leu Lys
                420   425   430

Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Ile His
        435   440   445

Gly Tyr Leu Gly Ile Val Glu Leu Leu Val Ser Leu Gly Ala Asp Val
        450   455   460

Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala Val
465   470   475   480

Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly Ala
                485   490   495

Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu Thr
          500   505   510

Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln Leu Thr
        515   520   525

Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser Tyr
    530   535   540

Asp Thr Glu Ser Glu Phe Thr Glu Phe Thr Glu Asp Glu Leu Pro Tyr
545   550   555   560

Asp Asp Cys Val Phe Gly Gly Gln Arg Leu Thr Leu
              565   570

<210> 3
<211> 2583
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

<400> 3
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aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180
gtcactactt tcggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240
catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tatttttttc 300
aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaaggtga taccttagtt 360
aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420
ttggaataca ctataactca tcacaatgtt tacatcatgg ctgacaaaca aaagaatggt 480
atcaaagtta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 540
cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 600
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gagtcagatc aagtggaatt gtgtggaacat cttatatccc aaatgtgtca ttaccaacat 1260
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<210> 4
<211> 860
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

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 1               5                  10                  15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
 65                  70                  75                  80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175
```

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180   185   190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
            195   200   205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
            210   215   220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Gln
225   230   235   240

Ser Pro Pro Pro Lys Lys Lys Arg Lys Val Glu Leu Gly Gly Ser Met
                    245   250   255

Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met Cys
            260   265   270

Ser Met Pro Arg Ser Leu Trp Leu Gly Cys Ser Ser Leu Ala Asp Ser
            275   280   285

Met Pro Ser Leu Arg Cys Leu Tyr Asn Pro Gly Thr Gly Ala Leu Thr
            290   295   300

Ala Phe Gln Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro
305   310   315   320

Pro Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn
                    325   330   335

Ser Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser
            340   345   350

Thr Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn
            355   360   365

Gly Thr Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser
            370   375   380

Tyr Glu Lys Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser
385   390   395   400

Glu Ser Asp Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys
                    405   410   415

His Tyr Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln
            420   425   430

Arg Asp Phe Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala
            435   440   445

Glu Asn Ile Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu
            450   455   460

Leu Val Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp
465   470   475   480

Lys Lys Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly
              485   490   495

Leu Ala Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro
              500   505   510

Pro Asp Gly Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro
              515   520   525

Lys Ile Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly
              530   535   540

Arg His Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly
545   550   555   560

Val Tyr Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg
              565   570   575

Asp Asn Thr Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg
              580   585   590

Ile Leu Thr Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu
              595   600   605

Arg Val Ile Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp
              610   615   620

Val Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala
625   630   635   640

Val Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys
              645   650   655

Asp Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr
              660   665   670

Leu Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp
              675   680   685

Phe Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys
              690   695   700

Val Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His
705   710   715   720

Lys Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser
              725   730   735

Gly Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala
              740   745   750

Cys Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg
              755   760   765

Phe Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys
              770   775   780

Val Trp Asp Leu Val Ala